

CRF Errors Corrected by the STIC Systems Branch

1652/600 #16 Dmt 3-12-02

CRF Processing Date: 3/5/2002
 Edited by: AV
 Verified by: AV (STIC staff)

Serial Number: 09/529,043B

ENTERED

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MAR 7 2002

TECH CENTER 1800/2900

- ☐ Changed a file from non-ASCII to ASCII
- ☒ Changed the margins in cases where the sequence text was "wrapped" down to the next line.
- ☐ Edited a format error in the Current Application Data section, specifically: _____
- ☐ Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other _____
- ☐ Added the mandatory heading and subheadings for "Current Application Data".
- ☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.
- ☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically: _____
- ☐ Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were: _____
- ☐ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited: _____
- ☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.
- ☐ Inserted colons after headings/subheadings. Headings edited included: _____
- ☐ Deleted extra, invalid, headings used by an applicant, specifically: _____
- ☐ Deleted: ☐ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file; ☐ page numbers throughout text; ☐ other invalid text, such as _____
- ☐ Inserted mandatory headings, specifically: _____
- ☐ Corrected an obvious error in the response, specifically: _____
- ☐ Edited identifiers where upper case is used but lower case is required, or vice versa.
- ☐ Corrected an error in the Number of Sequences field, specifically: _____
- ☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.
- ☐ Deleted *ending* stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: _____
- ☐ Other: _____

*Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form. 3/1/95



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MAR -7 2002

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/529,043B

DATE: 03/05/2002

TIME: 12:56:41 TECH CENTER 1600/2900

Input Set : A:\PTO.AMC.TXT

Output Set: N:\CRF3\03052002\I529043B.raw

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4 <110> APPLICANT: Forschungszentrum Juelich GmbH
6 <120> TITLE OF INVENTION: Method for microbial production of amino acids of the
7   aspartate and/or glutamate family and agents which can
8   be used in said method
10 <130> FILE REFERENCE: 1
12 <140> CURRENT APPLICATION NUMBER: 09/529,043B
13 <141> CURRENT FILING DATE: 2000-04-03
15 <150> PRIOR APPLICATION NUMBER: PCT/EP98/06210
16 <151> PRIOR FILING DATE: 1998-09-30
18 <160> NUMBER OF SEQ ID NOS: 4
20 <170> SOFTWARE: PatentIn Ver. 2.1
22 <210> SEQ ID NO: 1
23 <211> LENGTH: 3728
24 <212> TYPE: DNA
25 <213> ORGANISM: Corynebacterium glutamicum
27 <220> FEATURE:
28 <221> NAME/KEY: CDS
29 <222> LOCATION: (165)..(3587)
30 <223> OTHER INFORMATION: pyruvate carboxylase
32 <400> SEQUENCE: 1
33 cgcaaccgtg cttgaagtcg tgcaggtcag gggagtgttg cccgaaaaca ttgagaggaa 60
35 aacaaaaacc gatgtttgat tgggggaatc gggggttacg atactaggac gcagtgactg 120
37 ctatcaccct tggcggctctc ttgttgaaag gaataattac tcta gtg tcg act cac 176
38                                     Val Ser Thr His
39                                     1
41 aca tct tca acg ctt cca gca ttc aaa aag atc ttg gta gca aac cgc 224
42 Thr Ser Ser Thr Leu Pro Ala Phe Lys Lys Ile Leu Val Ala Asn Arg
43   5          10          15          20
45 ggc gaa atc gcg gtc cgt gct ttc cgt gca gca ctc gaa acc ggt gca 272
46 Gly Glu Ile Ala Val Arg Ala Phe Arg Ala Ala Leu Glu Thr Gly Ala
47          25          30          35
49 gcc acg gta gct att tac ccc cgt gaa gat cgg gga tca ttc cac cgc 320
50 Ala Thr Val Ala Ile Tyr Pro Arg Glu Asp Arg Gly Ser Phe His Arg
51          40          45          50
53 tct ttt gct tct gaa gct gtc cgc att ggt acc gaa ggc tca cca gtc 368
54 Ser Phe Ala Ser Glu Ala Val Arg Ile Gly Thr Glu Gly Ser Pro Val
55          55          60          65
57 aag gcg tac ctg gac atc gat gaa att atc ggt gca gct aaa aaa gtt 416
58 Lys Ala Tyr Leu Asp Ile Asp Glu Ile Ile Gly Ala Ala Lys Lys Val
59          70          75          80
61 aaa gca gat gcc att tac ccg gga tac ggc ttc ctg tct gaa aat gcc 464
62 Lys Ala Asp Ala Ile Tyr Pro Gly Tyr Gly Phe Leu Ser Glu Asn Ala
63 85          90          95          100

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PATENT APPLICATION: US/09/529,043B

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65 cag ctt gcc cgc gag tgt gcg gaa aac ggc att act ttt att ggc cca 512
66 Gln Leu Ala Arg Glu Cys Ala Glu Asn Gly Ile Thr Phe Ile Gly Pro
67          105          110          115
69 acc cca gag gtt ctt gat ctc acc ggt gat aag tct cgc gcg gta acc 560
70 Thr Pro Glu Val Leu Asp Leu Thr Gly Asp Lys Ser Arg Ala Val Thr
71          120          125          130
73 gcc gcg aag aag gct ggt ctg cca gtt ttg gcg gaa tcc acc ccg agc 608
74 Ala Ala Lys Lys Ala Gly Leu Pro Val Leu Ala Glu Ser Thr Pro Ser
75          135          140          145
77 aaa aac atc gat gag atc gtt aaa agc gct gaa ggc cag act tac ccc 656
78 Lys Asn Ile Asp Glu Ile Val Lys Ser Ala Glu Gly Gln Thr Tyr Pro
79          150          155          160
81 atc ttt gtg aag gca gtt gcc ggt ggt ggc gga cgc ggt atg cgt ttt 704
82 Ile Phe Val Lys Ala Val Ala Gly Gly Gly Gly Arg Gly Met Arg Phe
83 165          170          175          180
85 gtt gct tca cct gat gag ctt cgc aaa tta gca aca gaa gca tct cgt 752
86 Val Ala Ser Pro Asp Glu Leu Arg Lys Leu Ala Thr Glu Ala Ser Arg
87          185          190          195
89 gaa gct gaa gcg gct ttc ggc gat ggc gcg gta tat gtc gaa cgt gct 800
90 Glu Ala Glu Ala Ala Phe Gly Asp Gly Ala Val Tyr Val Glu Arg Ala
91          200          205          210
93 gtg att aac cct cag cat att gaa gtg cag atc ctt ggc gat cac act 848
94 Val Ile Asn Pro Gln His Ile Glu Val Gln Ile Leu Gly Asp His Thr
95          215          220          225
97 gga gaa gtt gta cac ctt tat gaa cgt gac tgc tca ctg cag cgt cgt 896
98 Gly Glu Val Val His Leu Tyr Glu Arg Asp Cys Ser Leu Gln Arg Arg
99          230          235          240
101 cac caa aaa gtt gtc gaa att gcg cca gca cag cat ttg gat cca gaa 944
102 His Gln Lys Val Val Glu Ile Ala Pro Ala Gln His Leu Asp Pro Glu
103 245          250          255          260
105 ctg cgt gat cgc att tgt gcg gat gca gta aag ttc tgc cgc tcc att 992
106 Leu Arg Asp Arg Ile Cys Ala Asp Ala Val Lys Phe Cys Arg Ser Ile
107          265          270          275
109 ggt tac cag ggc gcg gga acc gtg gaa ttc ttg gtc gat gaa aag ggc 1040
110 Gly Tyr Gln Gly Ala Gly Thr Val Glu Phe Leu Val Asp Glu Lys Gly
111          280          285          290
113 aac cac gtc ttc atc gaa atg aac cca cgt atc cag gtt gag cac acc 1088
114 Asn His Val Phe Ile Glu Met Asn Pro Arg Ile Gln Val Glu His Thr
115          295          300          305
117 gtg act gaa gaa gtc acc gag gtg gac ctg gtg aag gcg cag atg cgc 1136
118 Val Thr Glu Glu Val Thr Glu Val Asp Leu Val Lys Ala Gln Met Arg
119          310          315          320
121 ttg gct gct ggt gca acc ttg aag gaa ttg ggt ctg acc caa gat aag 1184
122 Leu Ala Ala Gly Ala Thr Leu Lys Glu Leu Gly Leu Thr Gln Asp Lys
123 325          330          335          340
125 atc aag acc cac ggt gca gca ctg cag tgc cgc atc acc acg gaa gat 1232
126 Ile Lys Thr His Gly Ala Ala Leu Gln Cys Arg Ile Thr Thr Glu Asp
127          345          350          355
129 cca aac aac ggc ttc cgc cca gat acc gga act atc acc gcg tac cgc 1280

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130 Pro Asn Asn Gly Phe Arg Pro Asp Thr Gly Thr Ile Thr Ala Tyr Arg
131          360          365          370
133 tca cca ggc gga gct ggc gtt cgt ctt gac ggt gca gct cag ctc ggt 1328
134 Ser Pro Gly Gly Ala Gly Val Arg Leu Asp Gly Ala Ala Gln Leu Gly
135          375          380          385
137 ggc gaa atc acc gca cac ttt gac tcc atg ctg gtg aaa atg acc tgc 1376
138 Gly Glu Ile Thr Ala His Phe Asp Ser Met Leu Val Lys Met Thr Cys
139          390          395          400
141 cgt ggt tcc gac ttt gaa act gct gtt gct cgt gca cag cgc gcg ttg 1424
142 Arg Gly Ser Asp Phe Glu Thr Ala Val Ala Arg Ala Gln Arg Ala Leu
143 405          410          415          420
145 gct gag ttc acc gtg tct ggt gtt gca acc aac att ggt ttc ttg cgt 1472
146 Ala Glu Phe Thr Val Ser Gly Val Ala Thr Asn Ile Gly Phe Leu Arg
147          425          430          435
149 gcg ttg ctg cgg gaa gag gac ttc act tcc aag cgc atc gcc acc gga 1520
150 Ala Leu Leu Arg Glu Glu Asp Phe Thr Ser Lys Arg Ile Ala Thr Gly
151          440          445          450
153 ttc att gcc gat cac ccg cac ctc ctt cag gct cca cct gct gat gat 1568
154 Phe Ile Ala Asp His Pro His Leu Leu Gln Ala Pro Pro Ala Asp Asp
155          455          460          465
157 gag cag gga cgc atc ctg gat tac ttg gca gat gtc acc gtg aac aag 1616
158 Glu Gln Gly Arg Ile Leu Asp Tyr Leu Ala Asp Val Thr Val Asn Lys
159          470          475          480
161 cct cat ggt gtg cgt cca aag gat gtt gca gct cct atc gat aag ctg 1664
162 Pro His Gly Val Arg Pro Lys Asp Val Ala Ala Pro Ile Asp Lys Leu
163 485          490          495          500
165 cct aac atc aag gat ctg cca ctg cca cgc ggt tcc cgt gac cgc ctg 1712
166 Pro Asn Ile Lys Asp Leu Pro Leu Pro Arg Gly Ser Arg Asp Arg Leu
167          505          510          515
169 aag cag ctt ggc cca gcc gcg ttt gct cgt gat ctc cgt gag cag gac 1760
170 Lys Gln Leu Gly Pro Ala Ala Phe Ala Arg Asp Leu Arg Glu Gln Asp
171          520          525          530
173 gca ctg gca gtt act gat acc acc ttc cgc gat gca cac cag tct ttg 1808
174 Ala Leu Ala Val Thr Asp Thr Thr Phe Arg Asp Ala His Gln Ser Leu
175          535          540          545
177 ctt gcg acc cga gtc cgc tca ttc gca ctg aag cct gcg gca gag gcc 1856
178 Leu Ala Thr Arg Val Arg Ser Phe Ala Leu Lys Pro Ala Ala Glu Ala
179          550          555          560
181 gtc gca aag ctg act cct gag ctt ttg tcc gtg gag gcc tgg ggc ggc 1904
182 Val Ala Lys Leu Thr Pro Glu Leu Leu Ser Val Glu Ala Trp Gly Gly
183 565          570          575          580
185 gcg acc tac gat gtg gcg atg cgt ttc ctc ttt gag gat ccg tgg gac 1952
186 Ala Thr Tyr Asp Val Ala Met Arg Phe Leu Phe Glu Asp Pro Trp Asp
187          585          590          595
189 agg ctc gac gag ctg cgc gag gcg atg ccg aat gta aac att cag atg 2000
190 Arg Leu Asp Glu Leu Arg Glu Ala Met Pro Asn Val Asn Ile Gln Met
191          600          605          610
193 ctg ctt cgc ggc cgc aac acc gtg gga tac acc ccg tac cca gac tcc 2048
194 Leu Leu Arg Gly Arg Asn Thr Val Gly Tyr Thr Pro Tyr Pro Asp Ser

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195          615          620          625
197 gtc tgc cgc gcg ttt gtt aag gaa gct gcc agc tcc ggc gtg gac atc 2096
198 Val Cys Arg Ala Phe Val Lys Glu Ala Ala Ser Ser Gly Val Asp Ile
199          630          635          640
201 ttc cgc atc ttc gac gcg ctt aac gac gtc tcc cag atg cgt cca gca 2144
202 Phe Arg Ile Phe Asp Ala Leu Asn Asp Val Ser Gln Met Arg Pro Ala
203 645          650          655          660
205 atc gac gca gtc ctg gag acc aac acc gcg gta gcc gag gtg gct atg 2192
206 Ile Asp Ala Val Leu Glu Thr Asn Thr Ala Val Ala Glu Val Ala Met
207          665          670          675
209 gct tat tct ggt gat ctc tct gat cca aat gaa aag ctc tac acc ctg 2240
210 Ala Tyr Ser Gly Asp Leu Ser Asp Pro Asn Glu Lys Leu Tyr Thr Leu
211          680          685          690
213 gat tac tac cta aag atg gca gag gag atc gtc aag tct ggc gct cac 2288
214 Asp Tyr Tyr Leu Lys Met Ala Glu Ile Val Lys Ser Gly Ala His
215          695          700          705
217 atc ttg gcc att aag gat atg gct ggt ctg ctt cgc cca gct gcg gta 2336
218 Ile Leu Ala Ile Lys Asp Met Ala Gly Leu Leu Arg Pro Ala Ala Val
219          710          715          720
221 acc aag ctg gtc acc gca ctg cgc cgt gaa ttc gat ctg cca gtg cac 2384
222 Thr Lys Leu Val Thr Ala Leu Arg Arg Glu Phe Asp Leu Pro Val His
223 725          730          735          740
225 gtg cac acc cac gac act gcg ggt ggc cag ctg gca acc tac ttt gct 2432
226 Val His Thr His Asp Thr Ala Gly Gly Gln Leu Ala Thr Tyr Phe Ala
227          745          750          755
229 gca gct caa gct ggt gca gat gct gtt gac ggt gct tcc gca cca ctg 2480
230 Ala Ala Gln Ala Gly Ala Asp Ala Val Asp Gly Ala Ser Ala Pro Leu
231          760          765          770
233 tct ggc acc acc tcc cag cca tcc ctg tct gcc att gtt gct gca ttc 2528
234 Ser Gly Thr Thr Ser Gln Pro Ser Leu Ser Ala Ile Val Ala Ala Phe
235          775          780          785
237 gcg cac acc acc cgt cgc gat acc ggt ttg agc ctc gag gct gtt tct gac 2576
238 Ala His Thr Arg Arg Asp Thr Gly Leu Ser Leu Glu Ala Val Ser Asp
239          790          795          800
241 ctc gag ccg tac tgg gaa gca gtg cgc gga ctg tac ctg cca ttt gag 2624
242 Leu Glu Pro Tyr Trp Glu Ala Val Arg Gly Leu Tyr Leu Pro Phe Glu
243 805          810          815          820
245 tct gga acc cca ggc cca acc ggt cgc gtc tac cgc cac gaa atc cca 2672
246 Ser Gly Thr Pro Gly Pro Thr Gly Arg Val Tyr Arg His Glu Ile Pro
247          825          830          835
249 ggc gga cag ttg tcc aac ctg cgt gca cag gcc acc gca ctg ggc ctt 2720
250 Gly Gly Gln Leu Ser Asn Leu Arg Ala Gln Ala Thr Ala Leu Gly Leu
251          840          845          850
253 gcg gat cgt ttc gaa ctc atc gaa gac aac tac gca gcc gtt aat gag 2768
254 Ala Asp Arg Phe Glu Leu Ile Glu Asp Asn Tyr Ala Ala Val Asn Glu
255          855          860          865
257 atg ctg gga cgc cca acc aag gtc acc cca tcc tcc aag gtt gtt ggc 2816
258 Met Leu Gly Arg Pro Thr Lys Val Thr Pro Ser Ser Lys Val Val Gly
259          870          875          880

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DATE: 03/05/2002

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Input Set : A:\PTO.AMC.TXT

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261 gac ctc gca ctc cac ctc gtt ggt gcg ggt gtg gat cca gca gac ttt 2864
262 Asp Leu Ala Leu His Leu Val Gly Ala Gly Val Asp Pro Ala Asp Phe
263 885 890 895 900
265 gct gcc gat cca caa aag tac gac atc cca gac tct gtc atc gcg ttc 2912
266 Ala Ala Asp Pro Gln Lys Tyr Asp Ile Pro Asp Ser Val Ile Ala Phe
267 905 910 915
269 ctg cgc ggc gag ctt ggt aac cct cca ggt ggc tgg cca gag cca ctg 2960
270 Leu Arg Gly Glu Leu Gly Asn Pro Pro Gly Gly Trp Pro Glu Pro Leu
271 920 925 930
273 cgc acc cgc gca ctg gaa ggc cgc tcc gaa ggc aag gca cct ctg acg 3008
274 Arg Thr Arg Ala Leu Glu Gly Arg Ser Glu Gly Lys Ala Pro Leu Thr
275 935 940 945
277 gaa gtt cct gag gaa gag cag gcg cac ctc gac gct gat gat tcc aag 3056
278 Glu Val Pro Glu Glu Glu Gln Ala His Leu Asp Ala Asp Asp Ser Lys
279 950 955 960
281 gaa cgt cgc aat agc ctc aac cgc ctg ctg ttc ccg aag cca acc gaa 3104
282 Glu Arg Arg Asn Ser Leu Asn Arg Leu Leu Phe Pro Lys Pro Thr Glu
283 965 970 975 980
285 gag ttc ctc gag cac cgt cgc cgc ttc ggc aac acc tct gcg ctg gat 3152
286 Glu Phe Leu Glu His Arg Arg Arg Phe Gly Asn Thr Ser Ala Leu Asp
287 985 990 995
289 gat cgt gaa ttc ttc tac ggc ctg gtc gaa ggc cgc gag act ttg atc 3200
290 Asp Arg Glu Phe Phe Tyr Gly Leu Val Glu Gly Arg Glu Thr Leu Ile
291 1000 1005 1010
293 cgc ctg cca gat gtg cgc acc cca ctg ctt gtt cgc ctg gat gcg atc 3248
294 Arg Leu Pro Asp Val Arg Thr Pro Leu Leu Val Arg Leu Asp Ala Ile
295 1015 1020 1025
297 tct gag cca gac gat aag ggt atg cgc aat gtt gtg gcc aac gtc aac 3296
298 Ser Glu Pro Asp Asp Lys Gly Met Arg Asn Val Val Ala Asn Val Asn
299 1030 1035 1040
301 ggc cag atc cgc cca atg cgt gtg cgt gac cgc tcc gtt gag tct gtc 3344
302 Gly Gln Ile Arg Pro Met Arg Val Arg Asp Arg Ser Val Glu Ser Val
303 1045 1050 1055 1060
305 acc gca acc gca gaa aag gca gat tcc tcc aac aag ggc cat gtt gct 3392
306 Thr Ala Thr Ala Glu Lys Ala Asp Ser Ser Asn Lys Gly His Val Ala
307 1065 1070 1075
309 gca cca ttc gct ggt gtt gtc acc gtg act gtt gct gaa ggt gat gag 3440
310 Ala Pro Phe Ala Gly Val Val Thr Val Thr Val Ala Glu Gly Asp Glu
311 1080 1085 1090
313 gtc aag gct gga gat gca gtc gca atc atc gag gct atg aag atg gaa 3488
314 Val Lys Ala Gly Asp Ala Val Ala Ile Ile Glu Ala Met Lys Met Glu
315 1095 1100 1105
317 gca aca atc act gct tct gtt gac ggc aaa atc gat cgc gtt gtg gtt 3536
318 Ala Thr Ile Thr Ala Ser Val Asp Gly Lys Ile Asp Arg Val Val Val
319 1110 1115 1120
321 cct gct gca acg aag gtg gaa ggt ggc gac ttg atc gtc gtc gtt tcc 3584
322 Pro Ala Ala Thr Lys Val Glu Gly Gly Asp Leu Ile Val Val Val Ser
323 1125 1130 1135 1140
325 taa acctttctgt aaaaagcccc gcgtcttcct catggaggag gcggggcttt 3637

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VERIFICATION SUMMARY

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